*J. ROARK*

#9

1644

RAW SEQUENCE LISTING
PATENT APPLICATION:   US/09/484,577

DATE: 12/05/2000
TIME: 17:29:41

Input Set : A:\Sequence Listing for 07419-029001.txt
Output Set: N:\CRF3\12052000\I484577.raw

ENTERED
see p. 5

RECEIVED
DEC 15 2000
TECH CENTER 1600/2900

```
 4 <110> APPLICANT: Gordon, Lynn K.
 5           Goodglick, Lee
 6           Goldman, Melissa
 8 <120> TITLE OF INVENTION: NOVEL GENES AND POLYPEPTIDES FOR THE
 9           DIAGNOSIS OF GIANT CELL ARTERITIS
12 <130> FILE REFERENCE: 07419-029001
14 <140> CURRENT APPLICATION NUMBER: 09/484,577
15 <141> CURRENT FILING DATE: 2000-01-18
17 <160> NUMBER OF SEQ ID NOS: 16
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 682
23 <212> TYPE: DNA
24 <213> ORGANISM: HOMOSAPIEN
26 <400> SEQUENCE: 1
27 gatccccgct ttcgcgggga tgacagcggt actcaattca cgcgcagcga tgccagcgaa       60
28 ctaaacggag gatctcacga acatccgctc caaccccgac accacgctcc ccgccgtcac      120
29 gacaggctcg ctgccctcct cgcgcaagtt ctttgcaatc cctgaggccg cgcccgacat      180
30 ccgcgttccc ttgcgcgaga tcatcctgtc cgagggcgcc ggcgagccga acctgccggt      240
31 ctatgacacc tcgggcccct acaccgatcc ggccgtgacg atcgacgtca acagcggcct      300
32 gccgcgcaat cgcctcgcct gggtcaagga acgcggcggc gtcgaggaat atcaggccgc      360
33 accatcaagc cggaggacaa cggcaatgtc ggcgcatccc acgccgccaa ggcgttcacc      420
34 ggcaccacaa gccgctgcgc ggctcgacgg cacaagatca cccactcgag ttcgccgcgc      480
35 cggcattata ccaaggagat gatctacgtc gccgagcgtg agaatcttgg cgcaagcagc      540
36 agctgagcgc gccgaggccg gctgccgacg gaagagtttt ggcgccgcgg tgccggctta      600
37 ttacgccgga atttgtcgca agagatcgcg cggcggccat tatttccttt aaaattaaca      660
38 ttgccgagct tgaaccgatg aa                                             682
40 <210> SEQ ID NO: 2
41 <211> LENGTH: 92
42 <212> TYPE: PRT
43 <213> ORGANISM: HOMOSAPIEN
45 <400> SEQUENCE: 2
46 Leu Pro Ala Val Thr Thr Gly Ser Leu Pro Ser Ser Arg Lys Phe Phe
47 1               5                   10                  15
48 Ala Ile Pro Glu Ala Ala Pro Asp Ile Arg Val Pro Leu Arg Glu Ile
49             20                  25                  30
50 Ile Leu Ser Glu Gly Ala Gly Glu Pro Asn Leu Pro Val Tyr Asp Thr
51         35                  40                  45
52 Ser Gly Pro Tyr Thr Asp Pro Ala Val Thr Ile Asp Val Asn Ser Gly
53     50                  55                  60
54 Leu Pro Arg Asn Arg Leu Ala Trp Val Lys Glu Arg Gly Gly Val Glu
55 65                  70                  75                  80
56 Glu Tyr Gln Ala Ala Pro Ser Ser Arg Arg Thr Thr
57             85                  90
59 <210> SEQ ID NO: 3
60 <211> LENGTH: 501
61 <212> TYPE: DNA
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 62 <213> ORGANISM: HOMOSAPIEN
 64 <400> SEQUENCE: 3
 65 actctccagc ctctcaccga ggatgaagtc ggctcgtgaa gtggttgcgg tcggggcaa          60
 66 aacccgggac gagctggcct tcctgccggc cgccctcgaa attgtcgaga cgccgccatc        120
 67 tcccaccgcg agactcacgg ccgccttgct tgctgccttg ttctactgcg ccgtggcgtg        180
 68 ggcgggtctc ggcaggatcg acatcgttgc ttctgcatcc agaaagatcg tgccgggcga        240
 69 ccgtgtaaag ctggttcagc cgctcgaggt cggcgtggtg cgggccactc atgtccgcga        300
 70 tggccaaacc gtcaaggccg gcgagattct gatcgagctg gatccattcg cgggtggtgt        360
 71 ggatgttgcg ccccgtcaga ggtccatcac ggtgtcggcg ccccacggat cgccacacca        420
 72 tcttgtcgac ctttcttcac cgacgagtca ccgccgagtt gccgatattg cgtgatctta        480
 73 tcagaatgcg gcgatgatca t                                                   501
 75 <210> SEQ ID NO: 4
 76 <211> LENGTH: 124
 77 <212> TYPE: PRT
 78 <213> ORGANISM: HOMOSAPIEN
 80 <400> SEQUENCE: 4
 81 Leu Ser Ser Leu Ser Pro Arg Met Lys Ser Ala Arg Glu Val Val Ala
 82  1               5                   10                  15
 83 Val Gly Gly Lys Thr Arg Asp Glu Leu Ala Phe Leu Pro Ala Ala Leu
 84              20                  25                  30
 85 Glu Ile Val Glu Thr Pro Pro Ser Pro Thr Ala Arg Leu Thr Ala Ala
 86          35                  40                  45
 87 Leu Leu Ala Ala Leu Phe Tyr Cys Ala Val Ala Trp Ala Gly Leu Gly
 88      50                  55                  60
 89 Arg Ile Asp Ile Val Ala Ser Ala Ser Arg Lys Ile Val Pro Gly Asp
 90 65                  70                  75                  80
 91 Arg Val Lys Leu Val Gln Pro Leu Glu Val Gly Val Val Arg Ala Thr
 92              85                  90                  95
 93 His Val Arg Asp Gly Gln Thr Val Lys Ala Gly Glu Ile Leu Ile Glu
 94              100                 105                 110
 95 Leu Asp Pro Phe Ala Gly Gly Val Asp Val Ala Thr
 96          115                 120
 98 <210> SEQ ID NO: 5
 99 <211> LENGTH: 747
100 <212> TYPE: DNA
101 <213> ORGANISM: HOMOSAPIEN
103 <400> SEQUENCE: 5
104 accgacgtcg actatccatg aacggatccc tgcaacgaca tcgtgcgtac ggcctatgaa         60
105 gcgctcgccg ccgtgctcgg tggcacgcag tcgctccaca ccaactcgtt cgacgaggcg        120
106 atcgcgctgc cgattgactt ctccgcccgg atcgcccgca acaccagctg atccagcagc        180
107 acgagacaga cgtcacggac gcggtcgaca ctctggcggg gtcctactac gtggagcgcc        240
108 tgacggatga cctcgccaag cgggcctggg agctgatgga agaggtcgag aagatgggtg        300
109 gcatggcgca ggcgatcgcg accggttggc cgaagcgcct gatcgagcaa tctgcgacgc        360
110 aaaagcaggc cgcgatcgat cgcggccgatc aggtgatcgt gggcgtgaac cgctaccggc        420
111 ccgaacagga gcaaccgatc gacattattg agatcgacaa ctcgacggtt cgggcctccc        480
112 agatccggtg tctcgccgaa atcgaaaagg cgcgtgattc aaggaaggtt gagtccgcgc        540
113 tcgggagct ggcgtgtatt gcccgcacgg gtgagggaaa tctgctggct gcagcgaccg        600
114 agcccgctcg cgcgcgggct accgtcgggg agatgtccga cgccatgcgg caagcattcg        660
115 gcgaccacga ggcggtgccg gaggtagtgt cggacgttta cggccgtgcc tatggcacgg        720
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116 atccgttcat ggatagtcga cgtcggt
118 <210> SEQ ID NO: 6                                              747
119 <211> LENGTH: 48
120 <212> TYPE: PRT
121 <213> ORGANISM: HOMOSAPIEN
123 <400> SEQUENCE: 6
124 Asp Pro Cys Asn Asp Ile Val Arg Thr Ala Tyr Glu Ala Leu Ala Ala
125 1               5                  10                  15
126 Val Leu Gly Gly Thr Gln Ser Leu His Thr Asn Ser Phe Asp Glu Ala
127             20                  25                  30
128 Ile Ala Leu Pro Ile Asp Phe Ser Ala Arg Ile Ala Arg Asn Thr Ser
129         35                  40                  45
131 <210> SEQ ID NO: 7
132 <211> LENGTH: 301
133 <212> TYPE: DNA
134 <213> ORGANISM: HOMOSAPIEN
136 <400> SEQUENCE: 7
137 actctccagc ctctcaccga ggatcatcga cgacattaag cagctggccg acaacggcgt
138 gcgcgaattc acgctgatcg gacagaatgt caacgcctac cacggcggag ggcccgacgg    60
139 ccgcgtctgg ccgctcggca aattgctgca gcgactcgcg gacattccag gcgtcatgcg   120
140 gctgcgttat tcgatcagcc atccgcgcga cgtcgacgac agcctgatcg ccgcgcatcg   180
141 cgatttgccc ggactgatgc cgttcgtgca cctgccggtg caatcggggg cggaccggat   240
142 c                                                                   300
                                                                        301
144 <210> SEQ ID NO: 8
145 <211> LENGTH: 91
146 <212> TYPE: PRT
147 <213> ORGANISM: HOMOSAPIEN
149 <400> SEQUENCE: 8
150 Ile Ile Asp Asp Ile Lys Gln Leu Ala Asp Asn Gly Val Arg Glu Phe
151 1               5                  10                  15
152 Thr Leu Ile Gly Gln Asn Val Asn Ala Tyr His Gly Gly Gly Pro Asp
153             20                  25                  30
154 Gly Arg Val Trp Pro Leu Gly Lys Leu Leu Gln Arg Leu Ala Asp Ile
155         35                  40                  45
156 Pro Gly Val Met Arg Leu Arg Tyr Ser Ile Ser His Pro Arg Asp Val
157     50                  55                  60
158 Asp Asp Ser Leu Ile Ala Ala His Arg Asp Leu Pro Gly Leu Met Pro
159 65              70                  75                  80
160 Phe Val His Leu Pro Val Gln Ser Gly Ala Asp
161             85                  90
163 <210> SEQ ID NO: 9
164 <211> LENGTH: 620
165 <212> TYPE: DNA
166 <213> ORGANISM: HOMOSAPIEN
168 <220> FEATURE:
169 <221> NAME/KEY: misc_feature
170 <222> LOCATION: (1)...(620)
171 <223> OTHER INFORMATION: n = A,T,C or G
173 <400> SEQUENCE: 9
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W--> 174 actctccanc ctctcaccga ggatcagaat aggtgaagag cgaagacacc gagaacgtct
     175 ggccttgaac ggacagcgtg cttgagttgg tcggggtcac caccggaccc gtgtccaccg      60
W--> 176 gcgcagtcac ngtgaaagca cttgaccatg atcccagacg gtgccgtcat ccgcgcggac     120
W--> 177 ccacancgtn tccgcgcccg accggattga tagctcagcg acaccagctg ggctgccgtg     180
W--> 178 acgtanttgt gctggttngg tgcaagtgcc accccgctca agacaaantg gccgcacctg     240
W--> 179 tgcccgtgtc ccaaacgtca tattgggtcg cagcactgtc gaacggatca ctgtangtgc     300
W--> 180 acagcgacna anccgcatan ctctngccgt ggggcgcaac gatgttnnac accgtctcaa     360
W--> 181 cgggtaccgt gtcnagggga ncatttacng ggaaagcatt cgaccactcc cccacaccgt     420
W--> 182 gcccgcattt gcgccgattc ctttcattga tatgtccacg tcggtnggnc tttaagcngg     480
W--> 183 cggcaaccgc ggtgnagctn cacttttgt tccttttatt ganggttaat ttgcgcgctt     540
W--> 184 tggncgtaan tntttngaan                                                600
                                                                           620
     186 <210> SEQ ID NO: 10
     187 <211> LENGTH: 662
     188 <212> TYPE: DNA
     189 <213> ORGANISM: HOMOSAPIEN
     191 <220> FEATURE:
     192 <221> NAME/KEY: misc_feature
     193 <222> LOCATION: (1)...(662)
     194 <223> OTHER INFORMATION: n = A,T,C or G
     196 <400> SEQUENCE: 10
     197 gatccgacca gcaatcaggc ggagctgcag cacctgaaaa acgaccttct ctcggcactg
     198 ctgggtattt cacgcaaccg ctctgcgctt ggcgggaaac accgacgcgc ttgaaggctt      60
     199 accggacgac acgccgccag ccttgattcg aatgcatctg gagtacttgc gcagtcagga     120
     200 ttccgagcag cgcgccaagc tgtccgaact ggatcagcaa cgggtgcaga aggtcgcgga     180
W--> 201 gaccaggacg atcgacgcca gcatcgcgaa gattgaagct ttgctgcggt gctgcaggan     240
     202 cgggtcgggg ttcgcaagta cctggcggac agggagtacg gctcaaagct gcaatattcg     300
     203 caggaactcc aggaactggt cgggatgcag caggacatcc tggtgcaacg gagcaaagct     360
W--> 204 cgaggaaacc aatgcggntt gtcgccgcac ttcgacgaaa acccgcggna agcttcgtct     420
W--> 205 nngaataacc ggcacccgnc tgttccnacg atcttggccc aaggggcacg aaaaaagggc     480
W--> 206 cggcaagncc tcaaaggacc aagggngttt taaaanccga gcacccggga cccaaccttt     540
W--> 207 aaaaancntt ggcggccccc attcgacggn gtggnggcaa caaattgggc cgngccccat     600
     208 tt                                                                     660
                                                                           662
     210 <210> SEQ ID NO: 11
     211 <211> LENGTH: 242
     212 <212> TYPE: DNA
     213 <213> ORGANISM: HOMOSAPIEN
     215 <220> FEATURE:
     216 <221> NAME/KEY: misc_feature
     217 <222> LOCATION: (1)...(242)
     218 <223> OTHER INFORMATION: n = A,T,C or G
     220 <400> SEQUENCE: 11
W--> 221 actctcnngc ctctcaccga agatagccgg caaggactgg cgngaacann gcgcgctgga
W--> 222 ctatcnctaa agggtctccn acnacgtcca nccggacnag ctgacctcgt ttccncnaag      60
W--> 223 cgtgaaactg aaggccggtg aaaccntcnt gttcgcctng atcacctact agtcgcgcgc     120
W--> 224 cnngcgcgac aggatcaacg ccaaggtgat ggccgatccc cgcctggcgt cgtcgatgga     180
     225 tc                                                                   240
                                                                           242
     227 <210> SEQ ID NO: 12
     228 <211> LENGTH: 552
     229 <212> TYPE: DNA
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RAW SEQUENCE LISTING
PATENT APPLICATION:   US/09/484,577        DATE: 12/05/2000
                                           TIME: 17:29:41

Input Set : A:\Sequence Listing for 07419-029001.txt
Output Set: N:\CRF3\12052000\I484577.raw

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230 <213> ORGANISM: HOMOSAPIEN
232 <400> SEQUENCE: 12
233 gatccgctcg atgcccaggc ccagtacagc gaactgttcg cccatggccg cgccacgtca        60
234 ctgttgctat tcgaacatgt tcacggtgaa tcccgtgacc gcggccaggc gatggtggac       120
235 ctgctggcgc agtacgagca gcacggtttg cagttaaaca gccgcgaatt accggaccac       180
236 ctgccgctgt atctggagta cctgtcgcag ctgccgcaag gcgaagccgt ggaaggtttg       240
237 aaagatatcg cgccgattct ggcattgctg agcgcgcgtc gcgaagccgt ggaaggtttg       240
238 tatgccgtga tgtttgatct gctgctgaaa ttggccgata ccgctatcga cagcgacaaa       300
239 gtggcggaaa aaattgccga cgaagcgcgc gatgatacgc cgcaggcgct ggatgctgtt       360
240 tgggaagaag agcaggttaa attctttgct gacaaaggct gcggcgattc agcaatcact       420
241 gctcatcagc gtcgctttgc cggtgccgtc gcgccgcaat atctgaatat cctcggtgag       480
242 aggctggaga gt                                                          540
                                                                         552
244 <210> SEQ ID NO: 13
245 <211> LENGTH: 265
246 <212> TYPE: DNA
247 <213> ORGANISM: HOMOSAPIEN
249 <220> FEATURE:
250 <221> NAME/KEY: misc_feature
251 <222> LOCATION: (1)...(265)    /
252 <223> OTHER INFORMATION: n = A,T,C or G
254 <400> SEQUENCE: 13
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W--> 255 gatcctnaca cantagcccg tggacgcatt tgcgtcgacc ctcatangga agcgatacga
W--> 256 ggcgggtnaa agtgaacatc cgccgagcac ggcagcgacg cctccgctca agcgtcngcgc    60
W--> 257 agtacttcct cgggtcgccg cgcctagcac tctgcgccgt gacatcaanc cgtgaaccca   120
W--> 258 cgggagactt tgcgccgcna agggatgagt ccactattag atgacgcatg gctacgagcc   180
W--> 259 natcctcggt ganaagctgg agagt                                        240
                                                                         265
261 <210> SEQ ID NO: 14
262 <211> LENGTH: 317
263 <212> TYPE: DNA
264 <213> ORGANISM: HOMOSAPIEN
266 <220> FEATURE:
267 <221> NAME/KEY: misc_feature
268 <222> LOCATION: (1)...(317)    /
269 <223> OTHER INFORMATION: n = A,T,C or G
271 <400> SEQUENCE: 14
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```
W--> 272 gatccggccn cgcacganct taccggtnaa aacttccncn ccnataatat ttgccgcgcg
W--> 273 agccgccctg angctctcgg cgtaactccg gatgcacggg ggaccgtgac ggttgtantg    60
W--> 274 ccctggcttt tctcagcnga aatctgcaca gccatcttcc gatcgatctg gcgcaggtgg   120
W--> 275 ggcggcncaa aacggtgggc atctccaaac cgcaggaacg tgttttgcag gatgtcgaac   180
W--> 276 atcatccacg cttcggtncc caacggctac ttcgcccggt accgggccat gtcatcctcg   240
W--> 277 gtganaagct gganant                                                 300
                                                                         317
279 <210> SEQ ID NO: 15
280 <211> LENGTH: 341
281 <212> TYPE: DNA
282 <213> ORGANISM: HOMOSAPIEN
284 <220> FEATURE:
285 <221> NAME/KEY: misc_feature
286 <222> LOCATION: (1)...(341)    /
287 <223> OTHER INFORMATION: n = A,T,C or G
```

✓ F.Y.I.

**Please Note:**
Use of n and/or Xaa have been detected in the Sequence Listing.  Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION:  US/09/484,577

DATE: 12/05/2000
TIME: 17:29:42

Input Set : A:\Sequence Listing for 07419-029001.txt
Output Set: N:\CRF3\12052000\I484577.raw

L:174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16

RECEIVED

DEC 15

TECH... ... ...